

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,955

DATE: 07/27/2001

TIME: 19:56:41

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Output Set: N:\CRF3\07272001\I806955.raw

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3 <110> APPLICANT: Panayi, Gabriel S
4 Corrigall, Valerie M
5 Bodman-Smith, Mark D
6 Fife, Mark S
7 Lanchbury, Jeremy S
9 <120> TITLE OF INVENTION: Treatment of Inflammatory Disease
11 <130> FILE REFERENCE: infection
13 <140> CURRENT APPLICATION NUMBER: 09/806955
14 <141> CURRENT FILING DATE: 2001-04-06
16 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03316
17 <151> PRIOR FILING DATE: 1999-10-08
19 <150> PRIOR APPLICATION NUMBER: GB9822115.3
20 <151> PRIOR FILING DATE: 1998-10-09
22 <160> NUMBER OF SEQ ID NOS: 5
24 <170> SOFTWARE: PatentIn Ver. 2.0
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27 <211> LENGTH: 639
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39 35 40 45
41 Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
42 50 55 60
44 Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
45 65 70 75 80
47 Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
48 85 90 95
50 Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
51 100 105 110
53 Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
54 115 120 125
56 Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
57 130 135 140
59 Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
60 145 150 155 160
62 Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn
63 165 170 175
65 Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly
66 180 185 190
68 Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
69 195 200 205
71 Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe

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74 Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
75 225      230      235      240
77 Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
78      245      250      255
80 Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
81      260      265      270
83 Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
84      275      280      285
86 Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu
87      290      295      300
89 Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
90 305      310      315      320
92 Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
93      325      330      335
95 Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
96      340      345      350
98 Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro Ser Arg
99      355      360      365
101 Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
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104 Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
105 385      390      395      400
107 Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
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110 Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
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114      435      440      445
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117      450      455      460
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123      485      490      495
125 Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
126      500      505      510
128 Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
129      515      520      525
131 Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
132      530      535      540
134 Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp
135 545      550      555      560
137 Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu Thr Met
138      565      570      575
140 Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His Gln Asp
141      580      585      590
143 Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu Glu Ile
144      595      600      605

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162 Leu Gly Thr Thr Tyr Ser Cys Val Gly Val Phe Lys Asn Gly Arg Val
163      20      25      30
165 Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser Tyr Val
166      35      40      45
168 Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
169      50      55      60
171 Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
172 65      70      75      80
174 Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
175      85      90      95
177 Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
178      100     105     110
180 Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
181      115     120     125
183 Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
184      130     135     140
186 Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
187 145     150     155     160
189 Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn
190      165     170     175
192 Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly
193      180     185     190
195 Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
196      195     200     205
198 Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe
199      210     215     220
201 Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
202 225     230     235     240
204 Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
205      245     250     255
207 Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
208      260     265     270
210 Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
211      275     280     285
213 Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu
214      290     295     300
216 Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
217 305      310      315      320

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219 Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
220                               325                               330                               335
222 Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
223                               340                               345                               350
225 Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro Ser Arg
226                               355                               360                               365
228 Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
229                               370                               375                               380
231 Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
232 385                               390                               395                               400
234 Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
235                               405                               410                               415
237 Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
238                               420                               425                               430
240 Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys Val Tyr
241                               435                               440                               445
243 Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly Thr Phe
244                               450                               455                               460
246 Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu
247 465                               470                               475                               480
249 Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr Ala Glu
250                               485                               490                               495
252 Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
253                               500                               505                               510
255 Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
256                               515                               520                               525
258 Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
259                               530                               535                               540
261 Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp
262 545                               550                               555                               560
264 Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu Thr Met
265                               565                               570                               575
267 Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His Gln Asp
268                               580                               585                               590
270 Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu Glu Ile
271                               595                               600                               605
273 Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro Pro Pro
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277 625                               630
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281 <211> LENGTH: 1917
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288 aaccgcatca cgccgtccta tgtcgcttc actcctgaag gggaacgtct gattggcgat 180
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290 atcggccgca cgtggaatga cccgtctgtg cagcaggaca tcaagttctt gccgttcaag 300
291 gtggttgaaa agaaaactaa accatacatt caagttgata ttggagggtg gcaaacaaag 360
292 acatttgctc ctgaagaaat ttctgccatg gttctcacta aaatgaaaga aaccgctgag 420
293 gcttatttgg gaaagaaggt taccatgca gttgttactg taccagccta ttttaatgat 480
294 gcccaacgcc aagcaaccaa agacgctgga actattgctg gcctaaatgt tatgaggatc 540
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297 aatggtgtct tcgaagttgt ggccactaat ggagatactc atctgggtgg agaagacttt 720
298 gaccagcgtg tcatggaaca cttcatcaaa ctgtacaaaa agaagacggg caaagatgtc 780
299 aggaaagaca atagagctgt gcagaaactc cggcgcgagg tagaaaaggc caaacggggc 840
300 ctgtcttctc agcatcaagc aagaattgaa attgagtcct tctatgaagg agaagacttt 900
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316 aagaagaagg aactggaaga aattgttcaa ccaattatca gcaaactcta tgggaagtga 1860
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331 <211> LENGTH: 32
332 <212> TYPE: DNA
333 <213> ORGANISM: Artificial Sequence
335 <220> FEATURE:
336 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
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VERIFICATION SUMMARY

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